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```
=> s (cDNA or gDNA or sense or antisense)(5w)librar?
        142574 CDNA
            94 GDNA
         26656 SENSE
         26968 ANTISENSE
         63253 LIBRAR?
L1       23107 (CDNA OR GDNA OR SENSE OR ANTISENSE)(5W)LIBRAR?

=> s l1 and immobi?(6w)(solid or support or substrate)
        105541 IMMOBI?
        834411 SOLID
        330946 SUPPORT
        636617 SUBSTRATE
          5338 IMMOBI?(6W)(SOLID OR SUPPORT OR SUBSTRATE)
L2          21 L1 AND IMMOBI?(6W)(SOLID OR SUPPORT OR SUBSTRATE)
```

FILE 'MEDLINE' ENTERED AT 14:21:07 ON 06 MAR 2003

FILE LAST UPDATED: 5 MAR 2003 (20030305/UP). FILE COVERS 1958 TO DATE.

On June 9, 2002, MEDLINE was reloaded. See HELP RLOAD for details.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2003 vocabulary. See http://www.nlm.nih.gov/mesh/summ2003.html for a description on changes.

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```
=> s l1
         85279 CDNA
            55 GDNA
         27857 SENSE
         17505 ANTISENSE
         55813 LIBRAR?
L3       16247 (CDNA OR GDNA OR SENSE OR ANTISENSE)(5W)LIBRAR?

=> s l2
         85279 CDNA
            55 GDNA
         27857 SENSE
         17505 ANTISENSE
         55813 LIBRAR?
         16247 (CDNA OR GDNA OR SENSE OR ANTISENSE)(5W)LIBRAR?
         46857 IMMOBI?
         70638 SOLID
       3318048 SUPPORT
        152770 SUBSTRATE
           904 IMMOBI?(6W)(SOLID OR SUPPORT OR SUBSTRATE)
L4           4 L1 AND IMMOBI?(6W)(SOLID OR SUPPORT OR SUBSTRATE)
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FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 5 March 2003 (20030305/ED)

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=> s l1
         99547 CDNA
            77 GDNA
        194894 SENSE
         19854 ANTISENSE
         45349 LIBRAR?
L5       17172 (CDNA OR GDNA OR SENSE OR ANTISENSE)(5W)LIBRAR?

=> s l2
         99547 CDNA
            77 GDNA
        194894 SENSE
         19854 ANTISENSE
         45349 LIBRAR?
         17172 (CDNA OR GDNA OR SENSE OR ANTISENSE)(5W)LIBRAR?
         56797 IMMOBI?
         89596 SOLID
        502705 SUPPORT
        178277 SUBSTRATE
          1526 IMMOBI?(6W)(SOLID OR SUPPORT OR SUBSTRATE)
L6           4 L1 AND IMMOBI?(6W)(SOLID OR SUPPORT OR SUBSTRATE)

=> d l6 1-4 ti au so py ab
```

			combinatorial	
S1886	U	USPT,PGPB,JPAB,EPAB,DWPI,TDBD	(((JAK2 or (Janus activated kinase))and phospho$6)and nicotine receptor) and library adj3 (agonist or antagonist or peptide)	2003-03-03 14:39:45
S1885	U	USPT,PGPB,JPAB,EPAB,DWPI,TDBD	((JAK2 or (Janus activated kinase))and phospho$6) and nicotine receptor	2003-03-03 14:38:50
S1884	U	USPT,PGPB,JPAB,EPAB,DWPI,TDBD	(JAK2 or (Janus activated kinase)) and phospho$6	2003-03-03 14:38:14
S1883	U	USPT,PGPB,JPAB,EPAB,DWPI,TDBD	JAK2 or (Janus activated kinase)	2003-03-03 14:37:50
S1882	U	USPT,PGPB,JPAB,EPAB,DWPI,TDBD	(nicotine adj5 receptor) and library adj5(agonist or antagonist or modulator or disruptor or peptide)	2003-03-03 14:28:43
S1881	U	USPT,PGPB,JPAB,EPAB,DWPI,TDBD	nicotine adj5 receptor	2003-03-03 14:27:37
S1880	U	USPT	6100269.pn.	2003-03-01 20:55:55
S1879	U	USPT	6225077.pn.	2003-03-01 19:52:41
S1878	U	USPT,PGPB,JPAB,EPAB,DWPI,TDBD	((cDNA library) adj5 immobil$6 adj6 (solid or support or substrate)) and (RT or reverse transcriptase)	2003-03-01 15:23:32
S1877	U	USPT,PGPB,JPAB,EPAB,DWPI,TDBD	(cDNA library) adj5 immobil$6 adj6 (solid or support or substrate)	2003-03-01 15:22:52
S1876	U	USPT,PGPB,JPAB,EPAB,DWPI,TDBD	Librar$4 adj6 (antagonist or inhibitor or modulator) adj6 (nuclear or receptor	2003-02-27 11:29:16

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NEWS 11	Jun 10	PCTFULL has been reloaded
NEWS 12	Jul 02	FOREGE no longer contains STANDARDS file segment
NEWS 13	Jul 22	USAN to be reloaded July 28, 2002; saved answer sets no longer valid
NEWS 14	Jul 29	Enhanced polymer searching in REGISTRY
NEWS 15	Jul 30	NETFIRST to be removed from STN
NEWS 16	Aug 08	CANCERLIT reload
NEWS 17	Aug 08	PHARMAMarketLetter(PHARMAML) - new on STN
NEWS 18	Aug 08	NTIS has been reloaded and enhanced
NEWS 19	Aug 19	Aquatic Toxicity Information Retrieval (AQUIRE) now available on STN
NEWS 20	Aug 19	IFIPAT, IFICDB, and IFIUDB have been reloaded
NEWS 21	Aug 19	The MEDLINE file segment of TOXCENTER has been reloaded
NEWS 22	Aug 26	Sequence searching in REGISTRY enhanced
NEWS 23	Sep 03	JAPIO has been reloaded and enhanced
NEWS 24	Sep 16	Experimental properties added to the REGISTRY file
NEWS 25	Sep 16	CA Section Thesaurus available in CAPLUS and CA
NEWS 26	Oct 01	CASREACT Enriched with Reactions from 1907 to 1985
NEWS 27	Oct 21	EVENTLINE has been reloaded
NEWS 28	Oct 24	BEILSTEIN adds new search fields
NEWS 29	Oct 24	Nutraceuticals International (NUTRACEUT) now available on STN
NEWS 30	Oct 25	MEDLINE SDI run of October 8, 2002
NEWS 31	Nov 18	DKILIT has been renamed APOLLIT
NEWS 32	Nov 25	More calculated properties added to REGISTRY
NEWS 33	Dec 02	TIBKAT will be removed from STN
NEWS 34	Dec 04	CSA files on STN
NEWS 35	Dec 17	PCTFULL now covers WP/PCT Applications from 1978 to date
NEWS 36	Dec 17	TOXCENTER enhanced with additional content
NEWS 37	Dec 17	Adis Clinical Trials Insight now available on STN
NEWS 38	Dec 30	ISMEC no longer available
NEWS 39	Jan 13	Indexing added to some pre-1967 records in CA/CAPLUS
NEWS 40	Jan 21	NUTRACEUT offering one free connect hour in February 2003
NEWS 41	Jan 21	PHARMAML offering one free connect hour in February 2003
NEWS 42	Jan 29	Simultaneous left and right truncation added to COMPENDEX, ENERGY, INSPEC
NEWS 43	Feb 13	CANCERLIT is no longer being updated
NEWS 44	Feb 24	METADEX enhancements
NEWS 45	Feb 24	PCTGEN now available on STN
NEWS 46	Feb 24	TEMA now available on STN

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 NEWS 47  Feb 26  NTIS now allows simultaneous left and right truncation
 NEWS 48  Feb 26  PCTFULL now contains images
 NEWS 49  Mar 04  SDI PACKAGE for monthly delivery of multifile SDI results

 NEWS EXPRESS  January 6 CURRENT WINDOWS VERSION IS V6.01a,
               CURRENT MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
               AND CURRENT DISCOVER FILE IS DATED 01 OCTOBER 2002
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FILE COVERS 1907 - 27 Feb 2003 VOL 138 ISS 10
FILE LAST UPDATED: 27 Feb 2003  (20030227/ED)

  This file contains CAS Registry Numbers for easy and accurate
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=> s (cDNA or gDNA or sense or antisense)(5w)librar?
        142574 CDNA
            94 GDNA
         26656 SENSE
         26968 ANTISENSE
         63253 LIBRAR?
L1       23107 (CDNA OR GDNA OR SENSE OR ANTISENSE)(5W)LIBRAR?
```

```
=> s l1 and immobi?(6w)(solid or support or substrate)
        105541 IMMOBI?
        834411 SOLID
        330946 SUPPORT
        636617 SUBSTRATE
          5338 IMMOBI?(6W)(SOLID OR SUPPORT OR SUBSTRATE)
L2          21 L1 AND IMMOBI?(6W)(SOLID OR SUPPORT OR SUBSTRATE)

=> d l2 1-21 ti au so py ab

L2   ANSWER 1 OF 21  CA  COPYRIGHT 2003 ACS
TI   Methods for identifying ligands of G protein-coupled receptors (GPCRs)
     from translated cDNA libraries and therapeutic uses
IN   Nestor, John J.; Wilson, Carol J.; Cantley, Lewis C.; Yaffe, Michael B.;
     Guo, Ailan
SO   PCT Int. Appl., 80 pp.
     CODEN: PIXXD2
PY   2002
     2002
AB   The invention relates to methods for identifying natural and non-natural
     ligands that bind to G Protein-Coupled Receptors (GPCRs) including orphan
     GPCRs. Methods of the invention include solubilizing and immobilizing
     GPCRs to facilitate efficient ligand selection. Methods generally involve
     the steps of assocg. a GPCR having a functional conformation with a
     support, interacting a naturally-derived sample with the GPCR to bind a
     mol. in the sample to the GPCR and sepg. the mol. from the support.
     Solubilization or isolation conditions according to the invention provide
     a functional conformation of a GPCR and allow for identification of a
     ligand that binds to a GPCR of interest. For example, a GPCR which has
     been tagged with a binding tag is immobilized by the tag to a
     support such as an affinity resin. Size exclusion methodol. can
     be used to sep. a purified receptor bound ligand complex from unbound
     components after pre-incubating the receptor with the sample. The
     naturally-derived sample can be a tissue ext., or a set of at least two
     proteins encoded by a cDNA library derived from a
     tissue or from a cell. The high affinity ligand can be released using low
     pH or high salt conditions and the structure identified by sequencing or
     mass spectrometry. Identified mols. can be used to treat diseases
     directly or can be used to design or screen for other therapeutics, such
     as natural or non-natural agonists or antagonists of GPCRs. Methods
     according to the invention also are useful in the identification of a
     function of an orphan GPCR.

L2   ANSWER 2 OF 21  CA  COPYRIGHT 2003 ACS
TI   Filamentous fungi polynucleotide array for gene expression profiling
IN   Abe, Keietu; Gomi, Katuya; Nakajima, Tasuku; Yamagata, Yohei; Hasegawa,
     Humihiko; Iguchi, Yasutaka
SO   PCT Int. Appl., 62 pp.
     CODEN: PIXXD2
PY   2002
     2002
AB   A method of detecting gene expression comprising immobilizing a probe
     contg. a mold-origin nucleic acid sequence, hybridizing a labeled
     polynucleotide sample to be detected with the immobilized probe as
     described above, and then detecting a signal from the hybridization
     product thus obtained, is disclosed. Use of such microarray for drug
     screening is claimed. More specifically, cDNA libraries
     from Aspergillus cultured under following conditions, carbon source-contg.
     (eutrophic) culture, carbon source-deficient (oligotrophic) culture,
     maltose culture, solid culture, spore germination culture, alk. culture,
     high-temp. culture and low-temp. culture, are used as source of probes.
     Polynucleotides from Aspergillus, penicillium, fusarium, Trichoderma,
     Mucor, are immobilized on a solid support
     made of cellulose, nylon, glass, non-porous material, or porous material.
     After fluorescent labeling, radio labeling, electron labeling, the target
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polynucleotides are hybridized with the microarray. Anal. of gene expression profiles in A oryzae and A. niger using the microarray constructed, is described.

L2 ANSWER 3 OF 21 CA COPYRIGHT 2003 ACS
TI Linear isothermal strand displacement amplification of RNA sequences
IN Kurn, Nurith
SO PCT Int. Appl., 148 pp.
CODEN: PIXXD2
PY 2002
AB The invention provides methods for isothermal amplification of RNA. The methods are particularly suitable for amplifying a plurality of RNA species in a sample. The methods employ a composite primer, a second primer and strand displacement to generate multiple copies of DNA products comprising sequences complementary to an RNA sequence of interest. In another aspect, the methods employ a single primer (which is a composite primer) and strand displacement to generate multiple copies of DNA products comprising sequences complementary to an RNA sequence of interest. In some embodiments, a transcription step is included to generate multiple copies of sense RNA of an RNA sequence of interest. The methods are useful for prepn. of nucleic acid libraries and substrates for anal. of gene expression of cells in biol. samples. The invention also provides compns. and kits for practicing the amplification methods, as well as methods which use the amplification products.

L2 ANSWER 4 OF 21 CA COPYRIGHT 2003 ACS
TI Compounds based on prostate tumor proteins for immunodiagnosis of prostate cancer and methods for their use
IN Xu, Jiangchun; Dillon, Davin C.
SO U.S. Pat. Appl. Publ., 111 pp., Cont.-in-part of U.S. Ser. No. 20,747, abandoned.
CODEN: USXXCO
PY 2002
1999
2002
AB The invention concerns compds. and methods for diagnosing prostate cancer. The inventive compds. include polypeptides contg. at least a portion of a prostate tumor protein. The inventive polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. Nucleic acid sequences for prepg. probes, primers, and polypeptides are also provided. Prostate tumor polypeptides were isolated from a prostate tumor **cDNA library** after subtraction of a normal pancreas **cDNA library**. The cDNAs were sequenced and homol. studies were done. Tissue specificity of the polypeptides was also detd.

L2 ANSWER 5 OF 21 CA COPYRIGHT 2003 ACS
TI Microarrayed organization of transcription factor target genes
IN Burgess, Robert M., Jr.; Lunyak, Victoria; Noskin, Leonid
SO PCT Int. Appl., 56 pp.
CODEN: PIXXD2
PY 2002
2002
AB The following invention outlines methodologies for the construction and utilization of transcription factor direct target gene microarrays of both DNA and corresponding protein/peptide target origin. The technol. entails the array/microarray annotation and organization of transcription factor direct loci and corresponding protein products identified through modified and improved versions of chromosomal immunopptn. (ChIP) and mol. cloning procedures. In vivo cross-linkage of protein/DNA complexes is performed in cell lines expressing the protein of interest and immunopptn. of protein /chromosomal complexes is subsequently employed through the utilization of antibodies specific for the transcription factor . It allows for the formulation of physiol. directed arrays which result in a thorough, focused characterization of the genetic and biochem. regulation

occurring within a give population of cells or a given tissue. Arrays and microarrays of direct targets for any given transcription factor created utilizing this technol. are substantially more clin. relevant for purposes of medical diagnostics and patient prognostics than conventional microarrays due to the physiol. focused nature and the transcription factor targets. In addn., the characterization and array organization of transcription factor target protein products and the assessment of their interactions with other proteins and/or small mols. is of crit. importance for the purposes of understanding cellular and organismal biol. and ultimately the design of therapeutics for human anomalies.

L2 ANSWER 6 OF 21 CA COPYRIGHT 2003 ACS
TI Method of identification of differentially expressed mRNA using customized amplification libraries (CAL)
IN Alland, David; Bloom, Barry R.; Kramnik, Igor
SO U.S. Pat. Appl. Publ., 19 pp.
CODEN: USXXCO
PY 2001
2002
AB The method provided by the present invention sets forth a novel combination of methods and principles which allows for the rapid and accurate isolation and identification of a large no. of differentially expressed mRNAs. The inventors have termed the novel approach for studying differences in mRNA expression "differential expression using customized amplification libraries" (DECAL), that permits global comparisons of bacterial gene expression under varied growth conditions without a specific requirement for DNA arrays. The key feature of DECAL technol. is the ability to amplify by PCR a complex mixt. of expressed genes in a reproducible and representative manner without the confounding effects of rRNA or any other highly expressed gene product. The inventors have found that three steps are essential for this process: (i) removal of abundant sequences--in this case rRNA sequences; (ii) redn. in the complexity of the sequences and conversion of all cDNA sequences into fragments of similar size; and (iii) selecting sequences that amplify efficiently. DECAL accomplishes this by creating a customized amplification library (CAL) of genomic sequences that has been manipulated for optimal performance during PCR amplification. Instead of amplifying total cDNA sequences, cDNA is hybridized to an excess of CAL, nonhybridizing CAL sequences are removed and the remaining CAL sequences are amplified without altering their proportion representation. The inventors have herein demonstrated the applicability of the DECAL system to the study of Mycobacterium tuberculosis gene expression in response to the antibiotic, isoniazid.

L2 ANSWER 7 OF 21 CA COPYRIGHT 2003 ACS
TI Solid support microorganism capture for **cDNA** cloning from **cDNA libraries**
IN Takahashi, Isao
SO Jpn. Kokai Tokkyo Koho, 6 pp.
CODEN: JKXXAF
PY 2001
AB The invention provides a method and kit for cloning cDNAs from **cDNA libraries** using solid support to capture microorganisms harboring cDNA clones. Formation of a complex between biotin labeled anti-LPS Fab antibody and fluorescent labeled LPS antigen, and avidin coated support, is described. Binding of E. coli displaces the fluorescent label and allows isolation of cDNA contg. E. coli via fluorescence-activated cell sorting (FACS).

L2 ANSWER 8 OF 21 CA COPYRIGHT 2003 ACS
TI Methods for generating enzymes using nucleic acid-protein fusion approaches
IN Kurz, Markus; Lohse, Peter
SO PCT Int. Appl., 39 pp.
CODEN: PIXXD2

PY 2001
2001
2002

AB Disclosed herein are novel methods for the generation and identification of catalytic and autoproteolytic proteins (enzymes) using nucleic acid-protein fusion approaches. In a first aspect, the invention features a method that involves the steps of: (a) providing a candidate catalytic protein fusion mol., including a candidate catalytic protein linked to both its nucleic acid coding sequence and a substrate; and (b) detg. whether the candidate catalytic protein catalyzes a reaction of the substrate by assaying for an alteration in mol. size, charge, or conformation of the fusion mol., relative to an unreacted fusion mol., thereby identifying a nucleic acid mol. which encodes a catalytic protein. The alteration in mol. size, charge, or conformation of the reacted fusion mol. may be detected by an alteration in electrophoretic mobility or by column chromatog. (for example, by HPLC, FPLC, ion exchange column chromatog., or size exclusion chromatog. anal.). In a related aspect, the invention features another method for identifying a nucleic acid mol. which encodes a catalytic protein, the method involving the steps of: (a) providing a candidate catalytic protein fusion mol., including a candidate catalytic protein linked to both its nucleic acid coding sequence and a substrate; (b) allowing the candidate catalytic protein to catalyze a reaction of the substrate in soln.; (c) contacting the product of step (b) with a capture mol. that has specificity for and binds a reacted fusion mol., but not an unreacted fusion mol., the capture mol. being **immobilized** on a **solid support**; and (d) detecting the reacted fusion mol. in assocn. with the solid support, thereby identifying a nucleic acid mol. which encodes a catalytic protein. In a third aspect, the invention features yet another method for identifying a nucleic acid mol. which encodes a catalytic protein, the method involving the steps of: (a) providing a candidate catalytic protein fusion mol., including a candidate catalytic protein linked to both its nucleic acid coding sequence and a substrate, the substrate being covalently bonded to an affinity tag; (b) allowing the candidate catalytic protein to catalyze a reaction of the substrate in soln.; (c) contacting the product of step (b) with a capture mol. that is specific for the affinity tag, the capture mol. being **immobilized** on a **solid support**; and (d) detg. whether the fusion mol. is bound to the solid support, wherein the detn. that a fusion mol. is not bound to the solid support identifies a nucleic acid mol. which encodes a catalytic protein. In a fourth aspect, the invention features a further method for identifying a nucleic acid mol. which encodes a catalytic protein, the method involving the steps of: (a) providing a candidate catalytic protein fusion mol., including a candidate catalytic protein linked to both its nucleic acid coding sequence and a substrate; (b) allowing the candidate catalytic protein to catalyze a reaction of the substrate in soln. in the presence of an affinity tag, the reaction resulting in the covalent attachment of the affinity tag to the fusion mol.; (c) immunopptg. the product of step (b) with an antibody that is specific for the affinity tag; and (d) detecting the immunopptn. complex, thereby identifying the fusion mol. as having a nucleic acid mol. which encodes a catalytic protein. These methods may be used for the isolation of novel enzymes with tailor-made activities and substrate specificities from randomized peptide and protein libraries, or for the directed evolution of existing enzymes with improved catalytic features.

L2 ANSWER 9 OF 21 CA COPYRIGHT 2003 ACS
TI Solid phase selection of differentially expressed genes with limited sequence information
IN Albrecht, Glenn; Brenner, Sydney; Dubridge, Robert B.
SO U.S., 33 pp., Cont.-in-part of U.S. Ser. No. 5,222, abandoned.
CODEN: USXXAM
PY 2001
1999
1999

1999
1999
2002
2000
2002
2003
2000

AB The invention provides a method and materials for monitoring and isolating differentially expressed genes. In accordance with the method of the invention, differently labeled populations of DNAs from sources to be compared are competitively hybridized with ref. DNA cloned on solid phase supports, e.g. microparticles, to provide a differential expression library which, in the preferred embodiment, may be manipulated by fluorescence-activated cell sorting (FACS). Monitoring the relative signal intensity of the different fluoroscent labels on the microparticles permits quant. anal. of expression levels relative to the ref. DNA. Populations of microparticles having relative signal intensities of interest can be isolated by FACS and the attached DNAs identified by sequencing, such as with massively parallel signature sequencing (MPSS), or with conventional DNA sequencing protocols. Detailed exptl. protocols for the prepn. of probe libraries are given.

L2 ANSWER 10 OF 21 CA COPYRIGHT 2003 ACS

TI Patient-tailored cloning of allergens by phage display: Peanut (Arachis hypogaea) profilin, a food allergen derived from a rare mRNA

AU Kleber-Janke, T.; Crameri, R.; Scheurer, S.; Vieths, S.; Becker, W.-M.

SO Journal of Chromatography, B: Biomedical Sciences and Applications (2001), 756(1-2), 295-305
CODEN: JCBBEP; ISSN: 0378-4347

PY 2001

AB A peanut **cDNA** phage surface display **library** was constructed and screened for the presence of IgE-binding proteins. The authors used a serum from a peanut-sensitized individual with a low specific IgE level to peanut ext. and suffering from mild symptoms after peanut ingestion. A total of 1011 cDNA clones were screened by affinity selection towards serum IgE **immobilized** to **solid**-phase supports. After five rounds of selective enrichment, sequence detn. of 25 inserts derived from different clones revealed presence of a single cDNA species. The cDNA-encoded gene product, formally termed Ara h 5, shows up to 80% amino acid sequence identity to the well-known plant allergen profilin, a 14 kDa protein present only in low amt. in peanut exts. Immunoblot anal. of fifty sera from individuals sensitized to peanut showed that 16% had mounted a detectable IgE response to the newly identified peanut profilin. High-level expression as non-fusion protein in BL21 (DE3) was carried under control of the inducible T7 promoter. Peanut profilin was purified by affinity chromatog. on poly-(l-proline)-Sepharose and yielded 30 mg l-1 culture of highly pure recombinant allergen. In spite of the high level of up to 80% amino acid identity to other plant profilins, inhibition expts. with recombinant profilins of peanut, cherry, pear, celery and birch revealed marked differences regarding their IgE-binding capacity.

L2 ANSWER 11 OF 21 CA COPYRIGHT 2003 ACS

TI RNA **immobilization** on filter paper-based **support** for storage and use in RT-PCR, **cDNA** synthesis or **cDNA** **library** construction

IN Goldsborough, Mindy D.; Fox, Donna K.

SO PCT Int. Appl., 43 pp.
CODEN: PIXXD2

PY 2001
2001
2002
2002

AB The present invention relates to a solid medium or support for use in the storage (preferably the long term storage) of nucleic acids (e.g., DNA and

RNA, rRNA and mRNA), particularly poly A RNA or mRNA which comprise the use of this solid medium or support. In particular, the invention relates to a method for storage and transport of such nucleic acids on the solid medium, as well as to methods which involve either recovery of the nucleic acids from the solid medium, and/or the use or manipulation of the nucleic acids obtained from or contained by the solid medium. Such use or manipulation includes, for example, digestion (e.g. with one or more nucleases, exonucleases or endonucleases such as restriction enzymes), synthesis (e.g. with one or more polymerases and/or reverse transcriptases), amplification (e.g. by polymerase chain reaction with one or more polymerases), sequencing (e.g. with one or more polymerases), or transformation or transfection into one or more host cells using, for example, chem. competent or electrocompetent cells or using known transfection reagents and techniques. In a preferred aspect, such manipulation involves RT-PCR, **cDNA** synthesis or **cDNA library** construction from RNA obtained from or contained by the solid support. The preferred medium or support is a matrix which protects against degrdn. of nucleic acids incorporated onto the matrix. Such a matrix may comprise an absorbent cellulose-based matrix or paper, or a micromesh of synthetic plastic material such as those described in U.S. Patent No. 5,496,562 and 5,976,572. FTA paper (available from Life Technologies, Inc.) and derivs., variants and modifications thereof are included among such supports. The ability to archive biol. samples for subsequent nucleic acid anal. is essential for tissue specimens and forensic samples. FTA Card is a chem. treated filter paper designed for the collection and room temp. storage of biol. samples for subsequent DNA anal. Its usefulness for the preservation of biol. samples for subsequent RNA anal. was tested. Here, we demonstrate that RNA in biol. samples stored on FTA Cards is stable and can be used successfully for RT-PCR and northern blot anal. RNA stability depends on the storage temp. and the type of biol. specimen. RNA in mammalian cells stored on FTA Cards is stable for over one year at temps. at or below -20.degree. and for two to three months in samples stored at room temp. For plant leaf; longer storage times (> 5 days) require temps. at or below -70.degree. following sample application. FTA Cards may constitute a method not only for convenient collection and storage of biol. samples but also for rapid RT-PCR anal. of tissue and cell samples.

L2 ANSWER 12 OF 21 CA COPYRIGHT 2003 ACS

TI Protein-ribosome-mRNA display: affinity isolation of enzyme-ribosome-mRNA complexes and cDNA cloning in a single-tube reaction

AU Bieberich, Erhard; Kapitonov, Dmitri; Tencomnao, Tewin; Yu, Robert K.

SO Analytical Biochemistry (2000), 287(2), 294-298
CODEN: ANBCA2; ISSN: 0003-2697

PY 2000

AB An enzyme-ribosome-mRNA complex was specifically purified by binding to the **immobilized** enzyme **substrate** and the cDNA was cloned in a single-tube reaction by one-step reverse transcription-PCR. The ganglioside GM3, used by sialyltransferase II (ST-II) as a substrate, was coated on a 96-well microtiter plate and ST-II was in vitro transcribed and translated from a **cDNA library**. The isolation of an enzyme-specific protein-ribosome (PRIME) complex was achieved with as little as 0.1 ng ST-II-specific cDNA in 5 .mu.g of a total plasmid prepn. or with the cDNA prepd. from sublibraries previously inoculated at a d. of 2000 clones/culture well. The affinity purifn. of the PRIME complex was highly specific for GM3 and did not result in cDNA amplification when a different ganglioside (GM1) was used for coating of the microtiter plate. The amplified cDNA was used for cloning or a second round of ribosome display, providing a fast anal. of enzyme affinity to multiple substrates. PRIME display can be used for host-free **cDNA** cloning from mRNA or **cDNA libraries** and for binding site mapping of the in vitro translated protein. The use of a single-tube reaction in ligand-coated microtiter plates indicates the versatility of PRIME display for cDNA cloning by automated procedures. (c) 2000 Academic Press.

L2 ANSWER 13 OF 21 CA COPYRIGHT 2003 ACS
TI Methods for amplifying and detecting multiple polynucleotides on a solid phase support
IN Hu, Qianjin; Peng, Zaoyuan; Yu, Zailin
SO PCT Int. Appl., 51 pp.
CODEN: PIXXD2
PY 2001
2002
2001
2002
2002
AB Methods for solid phase polymerase-mediated amplification using immobilized primers on a microarray are provided for detecting and cloning multiple target polynucleotides. The methods, compns. and kits provided herein are useful for research and clin. applications, particularly for large scale assays of genetic information in biol. samples of interest. The methods involve: (a) **immobilization** of sequence-specific oligonucleotide primers on **solid**-phase supports or in microarrays; (b) hybridization of the immobilized primers with target polynucleotides which may be differentially labeled or; (c) hybridization of the immobilized primers with target polynucleotides and amplification of the hybridized target polynucleotides using a thermostable polymerase and labeled dNTPs or a secondary label or; (d) hybridization of the immobilized primers with target polynucleotides and amplification of the hybridized target polynucleotides using a thermostable polymerase and labeled universal soln.-phase primers or labeled soln.-phase sequence-specific primers. Methods may also involve detecting and comparing the expression patterns of multiple target polynucleotides from at least two different biol. sources. Detection of hybridized target polynucleotides may also involve secondary biochem. reactions such as immunoassays. Solid-phase PCR methods are illustrated by amplification of human G3PDH, PKC-.alpha., c-Raf, and cyclin A target cDNAs, individually or together on glass slides, and by gene expression anal. of the above four genes in mRNA from OVC1.1 ovarian carcinoma cells or a fetal brain **cDNA library**.

L2 ANSWER 14 OF 21 CA COPYRIGHT 2003 ACS
TI Human cDNA probe array for the detection of genes encoding receptors and proteins associated with cell proliferation
IN Bandman, Olga; Lal, Preeti; Hillman, Jennifer L.; Yue, Henry; Reddy, Roopa; Guegler, Karl J.; Baughn, Mariah R.
SO U.S., 104 pp.
CODEN: USXXAM
PY 2001
AB The present invention relates to a compn. comprising a plurality of polynucleotide probes for use as hybridizable array elements in a microarray. The present invention also relates to a method for selecting polynucleotide probes for the compn. Thus, the BRAITUT07 **cDNA library** was constructed from cancerous brain tissue obtained from a 32-yr-old Caucasian male. One hundred thirty-four cDNA sequences sere selected because they possess motifs, descriptions, domains, regions, or other patterns consistent with genes coding for proteins assocd. with cell proliferation or receptors. This cDNA subset may be **immobilized** on a **substrate** as array elements in a microarray for the detection of genes encoding receptors and proteins involved in cell proliferation.

L2 ANSWER 15 OF 21 CA COPYRIGHT 2003 ACS
TI Function-based gene discovery using unique oligonucleotide-tagged bar-coded vectors for clone tracking and automation in **cDNA library** screening
IN Cen, Hui; Sun, Shaojian
SO PCT Int. Appl., 68 pp.
CODEN: PIXXD2

PY 1999
1999

AB The present invention relates generally to the field of genomics. More particularly, the present invention relates to methods for function-based gene discovery. Genes are identified as having or being assocd. with a specific function, as participating in a specific functional pathway, or as being a member of a specific functional group, by functional expression in one or more biol. readout assays. This invention is based, at least in part, on the recognition that the signal-to-noise ratio of a readout assay used to screen a **cDNA library** can be significantly enhanced by methods which localize multiple mol. copies of each unique clone into discrete regions or compartments prior to functional expression. In one embodiment, this invention provides methods for in situ transfection of a sorted library in a "bar-coded" vector to carry out expression of genes from libraries being screened in readout cells. The vector "bar code" is an oligonucleotide sequence within the vector which is unique to each individual clone of a library. The bar code enables sorting of the library in phys. space by hybridization to nucleic acid arrays which are complementary to library bar code sequences. The bar code unique to each clone together with the unique position of each complementary bar code in a nucleic acid array provides a method for direct retrieval of a gene having a function of interest in any given readout assay. Further, each unique bar code can serve as a specific primer for PCR and/or sequencing of a desired clone in a library. It is the ability to detect a biol. readout in a readout cell line which enables the user to identify genes having specific functions. It is able to directly screen mammalian **cDNA libraries** with an av. size of 106 clones through automation. Digestion of vectors is involved with restriction endonucleases. The methods set forth herein are suitable for application in a high throughput format for identification of genes and their functions simultaneously. Discovery of new genes and their functions permits development of diagnostics for early detection of diseases. This method permits discovery of discovery of disease-assocd. genes and is suitable for use with **antisense libraries**
.

L2 ANSWER 16 OF 21 CA COPYRIGHT 2003 ACS
TI Subtractive hybridization method for isolation of differentially expressed sequences
IN Hampson, Ian Noel; Hampson, Lynne
SO PCT Int. Appl., 25 pp.
CODEN: PIXXD2
PY 1999
1999
2000

AB Claimed is a method of obtaining target nucleic sequences derived from genes differentially expressed in a test cell sample as compared to a ref. cell sample by the use of subtractive hybridization. The duplex mols. formed during the subtractive hybridization step are subjected to selective crosslinking and the unsubtracted, single stranded cDNA is used as a template to generate nucleic acid strands complementary thereto incorporating a binding ligand. These complementary strands are then **immobilized** on a **solid** phase **support** system having a specific binding partner for the ligand. The solid phase support system is then treated to remove non-bound nucleic acid and leave a pure sample of the bound complementary strand. This bound strand may be used as, or to generate, the target nucleic acid mols.

L2 ANSWER 17 OF 21 CA COPYRIGHT 2003 ACS
TI A system for stable indirect immobilization of multimeric recombinant proteins
AU Grob, Philipp; Baumann, Sigrid; Ackermann, Mathias; Suter, Mark
SO Immunotechnology (1998), 4(2), 155-163
CODEN: IOTEER; ISSN: 1380-2933
PY 1998

AB To perform an ELISA or for panning phage particles which display recombinant proteins, one of the reactants is **immobilized** on **solid** phase. Immobilization in ELISA is generally performed by passive adsorption of ligands to plastic. However, protein is denatured during the adsorption process. This may result in low efficiency interaction between ligands and receptors which depend on native structures. In contrast, indirect immobilization has been shown to prevent protein denaturation. The aim of this study was to develop a system that allows efficient and stable indirect immobilization of a variety of recombinant multimeric proteins to solid phase. A new vector was constructed which allows the expression of up to three proteins linked by the Jun/Fos leucine zipper. Purifn. of the resulting protein was achieved by Ni+ affinity chromatog. utilizing the 6xHis-ABP (albumin binding protein) protein fused to the N-terminus of the Jun polypeptide. The high binding affinity of ABP to rat serum albumin (RSA) was exploited for indirect **immobilization** of recombinant proteins to **solid** phase. In an enzyme linked assay, the binding of ABP to immobilized RSA was shown to be 10-1000 times more efficient than other immobilization systems. Using the ZZ IgG binding domain of staphylococcal protein A as bait, the RSA-ABP immobilization system was successfully used to screen and enrich IgG Fc encoding DNA fragments from a **cDNA** phage **library**. The newly designed vector termed pJuFoexpress allows prodn. and purifn. of multimeric protein complexes linked by the Jun/Fos leucine zipper. Without chem. modifications, the recombinant proteins can be **immobilized** indirectly to **solid** phase. The immobilization results in the stable display of native, biol. active proteins which can be used in ELISA and phage display systems.

L2 ANSWER 18 OF 21 CA COPYRIGHT 2003 ACS
TI Analyzing immobilized **cDNA libraries** by endonuclease cleavage, hybridization to sequence-specific primers, and identification of primer extension products
IN Schmidt, Gunter; Thompson, Andrew Hugin
SO PCT Int. Appl., 22 pp.
CODEN: PIXXD2
PY 1999
1999
2000
2001
AB Claimed are improved methods for analyzing populations of cDNA derived from polyadenylated mRNA by immobilization, cleavage, primer extension, and identification of extended products. The method provides for characterizing one or more nucleic acids, which method comprises **immobilizing** double-stranded nucleic acids on a **solid** phase support, cleaving the immobilized nucleic acids with an endonuclease such that each cleaved nucleic acid has a double-stranded portion, denaturing the cleaved nucleic acids to form single-stranded cleaved nucleic acid, hybridizing one or more oligonucleotide sequences to the resulting single-stranded cleaved nucleic acid, each oligonucleotide sequence comprising a pre-detd. recognition sequence situated such that it recognizes a sequence which was part of the double-stranded portion of the nucleic acid and a label specific to the recognition sequence, extending correctly hybridized oligonucleotide sequences along the single-stranded portion of the immobilized nucleic acid to form an extended strand, denaturing the extended strand from the immobilized strand and characterizing the immobilized nucleic acid by identifying the size of the extended strand and the identity of the recognition sequence.

L2 ANSWER 19 OF 21 CA COPYRIGHT 2003 ACS
TI Compounds based on prostate tumor proteins for immunodiagnosis of prostate cancer and methods for their use
IN Xu, Jiangchun; Dillon, Davin C.
SO PCT Int. Appl., 141 pp.
CODEN: PIXXD2
PY 1998

1999
1999
1998
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2000
2001

AB Compds. and methods for diagnosing prostate cancer are provided. The inventive compds. include polypeptides contg. at least a portion of a prostate tumor protein. The inventive polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. Nucleic acid sequences for prepg. probes, primers, and polypeptides are also provided. Prostate tumor polypeptides were isolated from a prostate tumor **cDNA library** after subtraction of a normal pancreas **cDNA library**. The cDNAs were sequenced and homol. studies were done. Tissue specificity of the polypeptides was also detd.

L2 ANSWER 20 OF 21 CA COPYRIGHT 2003 ACS
TI Affinity selection of eukaryotic mRNAs and full-length cDNAs by a cap retention procedure (capture)
AU Pelletier, Jerry
SO Current Innovations in Molecular Biology (1997), 4(Gene Cloning and Analysis), 81-97
CODEN: CIMBFC
PY 1997
AB The ability to generate complementary DNA (**cDNA**) **libraries** is one of the most fundamental procedures of contemporary mol. biol. A major concern of current methods is that the majority of cDNAs present in any given library are incomplete, rendering the characterization of genes an inefficient and time-consuming task. The authors have developed an affinity selection method to purify mRNAs via non-covalent capture of the 5' cap structure. This protocol can also be used to enrich reverse transcription reaction products for full-length cDNAs. The key features of this method are a bifunctional fusion protein that can be **immobilized** onto a **solid support** matrix and which binds 5' cap structures of eukaryotic mRNAs. Following first strand cDNA synthesis, a single strand specific nuclease is used to remove cap structures from incomplete mRNA:cDNA duplexes. Specific enrichment of complete mRNA:cDNA duplexes is then achieved using this novel affinity matrix. This method can be used to enrich for full-length cDNAs or cDNA clones having complete 5' ends and to generate **cDNA libraries** in which reverse transcribed products of polyadenylated and non-polyadenylated mRNAs are equally represented.

L2 ANSWER 21 OF 21 CA COPYRIGHT 2003 ACS
TI Display of expression products of **cDNA libraries** on phage surfaces. A versatile screening system for selective isolation of genes by specific gene-product/ligand interaction
AU Crameri, Reto; Jaussi, Rolf; Menz, Guenter; Blaser, Kurt
SO European Journal of Biochemistry (1994), 226(1), 53-8
CODEN: EJBCAI; ISSN: 0014-2956
PY 1994
AB Techniques for cloning cDNAs from bacteriophage libraries **immobilized** on **solid** supports are well established. However, these techniques do not allow selective enrichment of clones expressing proteins of interest. Screening of **cDNA libraries** would be simplified if the proteins encoded by cDNAs could be expressed on the surface of phage. Phage carrying genes encoding proteins for which a ligand is available can be selected directly by affinity interaction. The expression products from a **cDNA library** from Aspergillus fumigatus were displayed on the surface of the filamentous phage M13 and screened for gene products binding to human serum IgE. The phys. linkage of cDNA-encoded proteins to the genetic information required for their prodn., achieved by exploiting the high-affinity interaction of the Jun and Fos leucine zippers, allows

screening of up to 1 .times. 1010 independent clones in 50-.mu.L aliquots applied to a well of a microtiter plate coated with the ligand. Phage displaying IgE-binding proteins were selectively enriched 105-106-fold over nonspecific phage after 6 rounds of growth and selection. The apparent mol. mass of the proteins selected from the **cDNA library** was in the range 20-40 kDa. Restriction enzyme anal. and preliminary sequence detn. of 12 selected inserts revealed different sequences. The ability of the proteins to bind to human serum IgE was corroborated by ELISA and by Western-blot anal. The developed cloning strategy allows isolation of cDNAs encoding proteins for which a ligand is available and circumvents **immobilization** of the libraries on **solid**-phase supports which hamper selective enrichment of clones expressing the desired protein.

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=> file medline
COST IN U.S. DOLLARS                                    SINCE FILE      TOTAL
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 for a description on changes.

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         17505 ANTISENSE
         55813 LIBRAR?
L3       16247 (CDNA OR GDNA OR SENSE OR ANTISENSE)(5W)LIBRAR?

=> s l2
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         55813 LIBRAR?
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         46857 IMMOBI?
         70638 SOLID
       3318048 SUPPORT
        152770 SUBSTRATE
           904 IMMOBI?(6W)(SOLID OR SUPPORT OR SUBSTRATE)
L4           4 L1 AND IMMOBI?(6W)(SOLID OR SUPPORT OR SUBSTRATE)
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=> d l4 1-4 ti au so py ab

L4   ANSWER 1 OF 4     MEDLINE
TI   Patient-tailored cloning of allergens by phage display: peanut (Arachis
     hypogaea) profilin, a food allergen derived from a rare mRNA.
AU   Kleber-Janke T; Crameri R; Scheurer S; Vieths S; Becker W M
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SO JOURNAL OF CHROMATOGRAPHY. B, BIOMEDICAL SCIENCES AND APPLICATIONS, (2001 May 25) 756 (1-2) 295-305.
Journal code: 9714109. ISSN: 1387-2273.
PY 2001
AB A peanut **cDNA** phage surface display **library** was constructed and screened for the presence of IgE-binding proteins. We used a serum from a peanut-sensitized individual with a low specific IgE level to peanut extract and suffering from mild symptoms after peanut ingestion. A total of 10(11) cDNA clones were screened by affinity selection towards serum IgE **immobilized** to **solid**-phase supports. After five rounds of selective enrichment, sequence determination of 25 inserts derived from different clones revealed presence of a single cDNA species. The cDNA-encoded gene product, formally termed Ara h 5, shows up to 80% amino acid sequence identity to the well-known plant allergen profilin, a 14 kD protein present only in low amount in peanut extracts. Immunoblot analysis of fifty sera from individuals sensitized to peanut showed that 16% had mounted a detectable IgE response to the newly identified peanut profilin. High-level expression as non-fusion protein in BL21 (DE3) was carried under control of the inducible T7 promoter. Peanut profilin was purified by affinity chromatography on poly-(L-proline)-Sepharose and yielded 30 mg l(-1) culture of highly pure recombinant allergen. In spite of the high level of up to 80% amino acid identity to other plant profilins, inhibition experiments with recombinant profilins of peanut, cherry, pear, celery and birch revealed marked differences regarding their IgE-binding capacity.

L4 ANSWER 2 OF 4 MEDLINE
TI Protein-ribosome-mRNA display: affinity isolation of enzyme-ribosome-mRNA complexes and cDNA cloning in a single-tube reaction.
AU Bieberich E; Kapitonov D; Tencomnao T; Yu R K
SO ANALYTICAL BIOCHEMISTRY, (2000 Dec 15) 287 (2) 294-8.
Journal code: 0370535. ISSN: 0003-2697.
PY 2000
AB An enzyme-ribosome-mRNA complex was specifically purified by binding to the **immobilized** enzyme **substrate** and the cDNA was cloned in a single-tube reaction by one-step reverse transcription-PCR. The ganglioside GM3, used by sialyltransferase II (ST-II) as a substrate, was coated on a 96-well microtiter plate and ST-II was in vitro transcribed and translated from a **cDNA library**. The isolation of an enzyme-specific protein-ribosome (PRIME) complex was achieved with as little as 0.1 ng ST-II-specific cDNA in 5 microg of a total plasmid preparation or with the cDNA prepared from sublibraries previously inoculated at a density of 2000 clones/culture well. The affinity purification of the PRIME complex was highly specific for GM3 and did not result in cDNA amplification when a different ganglioside (GM1) was used for coating of the microtiter plate. The amplified cDNA was used for cloning or a second round of ribosome display, providing a fast analysis of enzyme affinity to multiple substrates. PRIME display can be used for host-free **cDNA** cloning from mRNA or **cDNA libraries** and for binding site mapping of the in vitro translated protein. The use of a single-tube reaction in ligand-coated microtiter plates indicates the versatility of PRIME display for cDNA cloning by automated procedures.

L4 ANSWER 3 OF 4 MEDLINE
TI A system for stable indirect immobilization of multimeric recombinant proteins.
AU Grob P; Baumann S; Ackermann M; Suter M
SO IMMUNOTECHNOLOGY, (1998 Oct) 4 (2) 155-63.
Journal code: 9511979. ISSN: 1380-2933.
PY 1998
AB BACKGROUND: To perform an ELISA or for panning phage particles which display recombinant proteins, one of the reactants is **immobilized** on **solid** phase. Immobilization in ELISA is generally performed

by passive adsorption of ligands to plastic. However, protein is denatured during the adsorption process. This may result in low efficiency interaction between ligands and receptors which depend on native structures. In contrast, indirect immobilization has been shown to prevent protein denaturation. OBJECTIVES: The aim was to develop a system that allows efficient and stable indirect immobilization of a variety of recombinant multimeric proteins to solid phase. RESULTS: A new vector was constructed which allows the expression of up to three proteins linked by the Jun/Fos leucine zipper. Purification of the resulting protein was achieved by Ni+ affinity chromatography utilizing the 6xHis-ABP (albumin binding protein) protein fused to the N-terminus of the Jun polypeptide. The high binding affinity of ABP to rat serum albumin (RSA) was exploited for indirect **immobilization** of recombinant proteins to **solid** phase. In an enzyme linked assay, the binding of ABP to immobilized RSA was shown to be 10-1000 times more efficient than other immobilization systems. Using the ZZ IgG binding domain of staphylococcal protein A as bait, the RSA-ABP immobilization system was successfully used to screen and enrich IgG Fc encoding DNA fragments from a **cDNA** phage **library**. CONCLUSION: The newly designed vector termed pJuFoexpress allows production and purification of multimeric protein complexes linked by the Jun/Fos leucine zipper. Without chemical modifications, the recombinant proteins can be **immobilized** indirectly to **solid** phase. The immobilization results in the stable display of native, biologically active proteins which can be used in ELISA and phage display systems.

L4 ANSWER 4 OF 4 MEDLINE

TI Display of expression products of **cDNA libraries** on phage surfaces. A versatile screening system for selective isolation of genes by specific gene-product/ligand interaction.

AU Crameri R; Jaussi R; Menz G; Blaser K

SO EUROPEAN JOURNAL OF BIOCHEMISTRY, (1994 Nov 15) 226 (1) 53-8. Journal code: 0107600. ISSN: 0014-2956.

PY 1994

AB Techniques for cloning cDNAs from bacteriophage libraries **immobilised** on **solid** supports are well established. However, these techniques do not allow selective enrichment of clones expressing proteins of interest. Screening of **cDNA libraries** would be simplified if the proteins encoded by cDNAs could be expressed on the surface of phage. Phage carrying genes encoding proteins for which a ligand is available can be selected directly by affinity interaction [Crameri, R. & Suter, M. (1993) Gene (Amst.) 137, 69-75]. The expression products from a **cDNA library** from Aspergillus fumigatus have been displayed on the surface of the filamentous phage M13 and screened for gene products binding to human serum IgE. The physical linkage of cDNA-encoded proteins to the genetic information required for their production, achieved by exploiting the high-affinity interaction of the Jun and Fos leucine zippers, allows screening of up to 1 x 10(10) independent clones in 50-microliters aliquots applied to a well of a microtiter plate coated with the ligand. Phage displaying IgE-binding proteins were selectively enriched 10(5)-10(6)-fold over non-specific phage after six rounds of growth and selection. The apparent molecular mass of the proteins selected from the **cDNA library** was in the range 20-40 kDa. Restriction enzyme analysis and preliminary sequence determination of 12 selected inserts revealed different sequences. The ability of the proteins to bind to human serum IgE was corroborated by enzyme-linked immunosorbent assay and by Western-blot analysis. The developed cloning strategy allows isolation of cDNAs encoding proteins for which a ligand is available and circumvents **immobilisation** of the libraries on **solid** -phase supports which hamper selective enrichment of clones expressing the desired protein.

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FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 5 March 2003 (20030305/ED)

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         19854 ANTISENSE
         45349 LIBRAR?
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        194894 SENSE
         19854 ANTISENSE
         45349 LIBRAR?
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         56797 IMMOBI?
         89596 SOLID
        502705 SUPPORT
        178277 SUBSTRATE
          1526 IMMOBI?(6W)(SOLID OR SUPPORT OR SUBSTRATE)
L6           4 L1 AND IMMOBI?(6W)(SOLID OR SUPPORT OR SUBSTRATE)

=> d l6 1-4 ti au so py ab
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L6 ANSWER 1 OF 4 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Patient-tailored cloning of allergens by phage display: Peanut (Arachis hypogaea) profilin, a food allergen derived from a rare mRNA.
AU Kleber-Janke, Tamara; Crameri, Reto; Scheurer, Stephan; Vieths, Stefan; Becker, Wolf-Meinhard (1)
SO Journal of Chromatography B, (25 May, 2001) Vol. 756, No. 1-2, pp. 295-305. print.
ISSN: 0378-4347.
PY 2001
AB A peanut **cDNA** phage surface display **library** was constructed and screened for the presence of IgE-binding proteins. We used a serum from a peanut-sensitized individual with a low specific IgE level to peanut extract and suffering from mild symptoms after peanut ingestion. A total of 1011 cDNA clones were screened by affinity selection towards serum IgE **immobilized** to **solid**-phase supports. After five rounds of selective enrichment, sequence determination of 25 inserts derived from different clones revealed presence of a single cDNA species. The cDNA-encoded gene product, formally termed Ara h 5, shows up to 80% amino acid sequence identity to the well-known plant allergen profilin, a 14 kD protein present only in low amount in peanut extracts. Immunoblot analysis of fifty sera from individuals sensitized to peanut showed that 16% had mounted a detectable IgE response to the newly identified peanut profilin. High-level expression as non-fusion protein in BL21 (DE3) was

carried under control of the inducible T7 promoter. Peanut profilin was purified by affinity chromatography on poly-(L-proline)-Sepharose and yielded 30 mg l-1 culture of highly pure recombinant allergen. In spite of the high level of up to 80% amino acid identity to other plant profilins, inhibition experiments with recombinant profilins of peanut, cherry, pear, celery and birch revealed marked differences regarding their IgE-binding capacity.

L6 ANSWER 2 OF 4 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Protein-ribosome-mRNA display: Affinity isolation of enzyme-ribosome-mRNA complexes and cDNA cloning in a single-tube reaction.
AU Bieberich, Erhard (1); Kapitonov, Dmitri (1); Tencomnao, Tewin (1); Yu, Robert K. (1)
SO Analytical Biochemistry, (December 15, 2000) Vol. 287, No. 2, pp. 294-298. print.
ISSN: 0003-2697.
PY 2000
AB An enzyme-ribosome-mRNA complex was specifically purified by binding to the **immobilized** enzyme **substrate** and the cDNA was cloned in a single-tube reaction by one-step reverse transcription-PCR. The ganglioside GM3, used by sialyltransferase II (ST-II) as a substrate, was coated on a 96-well microtiter plate and ST-II was in vitro transcribed and translated from a **cDNA library**. The isolation of an enzyme-specific protein-ribosome (PRIME) complex was achieved with as little as 0.1 ng ST-II-specific cDNA in 5 mug of a total plasmid preparation or with the cDNA prepared from sublibraries previously inoculated at a density of 2000 clones/culture well. The affinity purification of the PRIME complex was highly specific for GM3 and did not result in cDNA amplification when a different ganglioside (GM1) was used for coating of the microtiter plate. The amplified cDNA was used for cloning or a second round of ribosome display, providing a fast analysis of enzyme affinity to multiple substrates. PRIME display can be used for host-free **cDNA** cloning from mRNA or **cDNA libraries** and for binding site mapping of the in vitro translated protein. The use of a single-tube reaction in ligand-coated microtiter plates indicates the versatility of PRIME display for cDNA cloning by automated procedures.

L6 ANSWER 3 OF 4 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI A system for stable indirect immobilization of multimeric recombinant proteins.
AU Grob, Philipp; Baumann, Sigrid; Ackermann, Mathias; Suter, Mark (1)
SO Immunotechnology (Shannon), (Oct., 1998) Vol. 4, No. 2, pp. 155-163.
ISSN: 1380-2933.
PY 1998
AB Background: To perform an ELISA or for panning phage particles which display recombinant proteins, one of the reactants is **immobilized** on **solid** phase. Immobilization in ELISA is generally performed by passive adsorption of ligands to plastic. However, protein is denatured during the adsorption process. This may result in low efficiency interaction between ligands and receptors which depend on native structures. In contrast, indirect immobilization has been shown to prevent protein denaturation. Objectives: The aim was to develop a system that allows efficient and stable indirect immobilization of a variety of recombinant multimeric proteins to solid phase. Results: A new vector was constructed which allows the expression of up to three proteins linked by the Jun/Fos leucine zipper. Purification of the resulting protein was achieved by Ni+ affinity chromatography utilizing the 6xHis-ABP (albumin binding protein) protein fused to the N-terminus of the Jun polypeptide. The high binding affinity of ABP to rat serum albumin (RSA) was exploited for indirect **immobilization** of recombinant proteins to **solid** phase. In an enzyme linked assay, the binding of ABP to immobilized RSA was shown to be 10-1000 times more efficient than other immobilization systems. Using the ZZ IgG binding domain of staphylococcal protein A as bait, the RSA-ABP immobilization system was successfully used

to screen and enrich IgG Fc encoding DNA fragments from a **cDNA** phage **library**. Conclusion: The newly designed vector termed pJuFoexpress allows production and purification of multimeric protein complexes linked by the Jun/Fos leucine zipper. Without chemical modifications, the recombinant proteins can be **immobilized** indirectly to **solid** phase. The immobilization results in the stable display of native, biologically active proteins which can be used in ELISA and phage display systems.

L6 ANSWER 4 OF 4 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Display of expression products of **cDNA libraries** on phage surfaces: A versatile screening system for selective isolation of genes by specific gene-product/ligand interaction.
AU Crameri, Reto (1); Jaussi, Rolf; Menz, Gunter; Blaser, Kurt
SO European Journal of Biochemistry, (1994) Vol. 226, No. 1, pp. 53-58. ISSN: 0014-2956.
PY 1994
AB Techniques for cloning cDNAs from bacteriophage libraries **immobilised** on **solid** supports are well established. However, these techniques do not allow selective enrichment of clones expressing proteins of interest. Screening of **cDNA libraries** would be simplified if the proteins encoded by cDNAs could be expressed on the surface of phage. Phage carrying genes encoding proteins for which a ligand is available can be selected directly by affinity interaction (Crameri, R. & Suter, M. (1993) Gene (Amst.) 137, 69-75). The expression products from a **cDNA library** from Aspergillus fumigatus have been displayed on the surface of the filamentous phage M13 and screened for gene products binding to human serum IgE. The physical linkage of cDNA-encoded proteins to the genetic information required for their production, achieved by exploiting the high-affinity interaction of the Jun and Fos leucine zippers, allows screening of up to 1 times 10-10 independent clones in 50-mu-l aliquots applied to a well of a microtiter plate coated with the ligand. Phage displaying IgE-binding proteins were selectively enriched 10-5 -10-6-fold over non-specific phage after six rounds of growth and selection. The apparent molecular mass of the proteins selected from the **cDNA library** was in the range 20-40 kDa. Restriction enzyme analysis and preliminary sequence determination of 12 selected inserts revealed different sequences. The ability of the proteins to bind to human serum IgE was corroborated by enzyme-linked immunosorbent assay and by Western-blot analysis. The developed cloning strategy allows isolation of cDNAs encoding proteins for which a ligand is available and circumvents **immobilisation** of the libraries on **solid**-phase supports which hamper selective enrichment of clones expressing the desired protein.

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                   added to PHAR
 NEWS 17  May 15   MEDLINE file segment of TOXCENTER reloaded
 NEWS 18  May 15   Supporter information for ENCOMPPAT and ENCOMPLIT updated
 NEWS 19  May 19   Simultaneous left and right truncation added to WSCA
 NEWS 20  May 19   RAPRA enhanced with new search field, simultaneous left and
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                  right truncation
 NEWS 21  Jun 06  Simultaneous left and right truncation added to CBNB
 NEWS 22  Jun 06  PASCAL enhanced with additional data
 NEWS 23  Jun 20  2003 edition of the FSTA Thesaurus is now available
 NEWS 24  Jun 25  HSDB has been reloaded
 NEWS 25  Jul 16  Data from 1960-1976 added to RDISCLOSURE
 NEWS 26  Jul 21  Identification of STN records implemented
 NEWS 27  Jul 21  Polymer class term count added to REGISTRY
 NEWS 28  Jul 22  INPADOC: Basic index (/BI) enhanced; Simultaneous Left and
                  Right Truncation available
 NEWS 29  AUG 05  New pricing for EUROPATFULL and PCTFULL effective
                  August 1, 2003

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L1          14 (GDNA OR SDNA)(6W) LIBR?

=> d l1 1-14 ti au so py ab

L1   ANSWER 1 OF 14  CA  COPYRIGHT 2003 ACS on STN
TI   Differential diagnosis of Taenia saginata and Taenia solium infections:
     from DNA probes to polymerase chain reaction
AU   Gonzalez, Luis Miguel; Montero, Estrella; Sciutto, Edda; Harrison, Leslie
     J. S.; Parkhouse, R. Michael E.; Garate, Teresa
SO   Transactions of the Royal Society of Tropical Medicine and Hygiene (2002),
     96(Suppl. 1), 243-250
     CODEN: TRSTAZ; ISSN: 0035-9203
PY   2002
AB   The objective of this work was the rapid and easy differential diagnosis
```

of Taenia saginata and T. solium. First, a T. saginata size-selected genomic DNA (**gDNA**) **library** was constructed in the vector .lambda.gt10 using the 2-4 kb fraction from the parasite DNA digested with EcoR1, under 'star' conditions. After differential screening of the library and hybridization anal. with DNA from T. saginata, T. solium, T. taeniaeformis, T. crassiceps, and Echinococcus granulosus (bovine, porcine, and human), 2 recombinant phages were selected. They were designated HDP1 and HDP2. HDP1 reacted specifically with T. saginata DNA, and HDP2 recognized DNA from both T. saginata and T. solium. The 2 DNA probes were then sequenced and further characterized. HDP1 was a repetitive sequence with a 53 bp monomeric unit repeated 24 times in direct tandem along the 1272 bp fragment, while the 3954 by HDP2 was not a repetitive sequence. Using the sequencing data, oligonucleotides were designed and used in a polymerase chain reaction (PCR). The 2 selected oligonucleotides from probe HDP1 (PTs4F1 and PTs4R1) specifically amplified gDNA from T. saginata, but not T. solium or other related cestodes, with a sensitivity of <10 pg of T. saginata gDNA, about the quantity of DNA in one taeniid egg. The 3 oligonucleotides selected from the HDP2 sequence (PTs7S35F1, PTs7S35F2, and PTs7S35R1) allowed the differential amplification of gDNA from T. saginata, T. solium and E. granulosus in a multiplex PCR, again with a sensitivity of < 10 pg. These diagnostic tools have immediate application in the differential diagnosis of T. solium and T. saginata in humans and in the diagnosis of dubious cysts in the slaughterhouse. We also hope to apply them to epidemiol. surveys of, for example, soil and water in endemic areas.

L1 ANSWER 2 OF 14 CA COPYRIGHT 2003 ACS on STN
TI An integrated SSR and RFLP linkage map of Sorghum bicolor (L.) Moench
AU Bhattramakki, Dinakar; Dong, Jianmin; Chhabra, Ashok K.; Hart, Gary E.
SO Genome (2000), 43(6), 988-1002
CODEN: GENOE3; ISSN: 0831-2796
PY 2000
AB We report the development, testing, and use (for genetic mapping) of a large no. of polymerase chain reaction (PCR) primer sets that amplify DNA simple sequence repeat (SSR) loci of Sorghum bicolor (L.) Moench. Most of the primer sets were developed from clones isolated from two sorghum bacterial artificial chromosome (BAC) libraries and three enriched sorghum genomic-DNA (**gDNA**) **libraries**. A few were developed from sorghum DNA sequences present in public databases. The libraries were probed with radiolabeled di- and trinucleotide oligomers, the BAC libraries with four and six oligomers, resp., and the enriched **gDNA libraries** with four and three oligomers, resp. Both types of libraries were markedly enriched for SSRs relative to a size-fractionated **gDNA library** studied earlier. However, only 2% of the sequenced clones obtained from the size-fractionated **gDNA library** lacked a SSR, whereas 13% and 17% of the sequenced clones obtained from the BAC and enriched **gDNA libraries**, resp., lacked a SSR. Primer sets were produced for 313 SSR loci. Two-hundred sixty-six (85%) of the loci were amplified and 165 (53%) of the loci were found to be polymorphic in a population composed of 18 diverse sorghum lines. (AG/TC)n and (AC/TG)n repeats comprised 91% of the dinucleotide SSRs and 52% of all of the SSRs at the polymorphic loci, whereas four types of repeats comprised 66% of the trinucleotide SSRs at the loci. Primer sequences are reported for the 165 polymorphic loci and for eight monomorphic loci that have a high degree of homol. to genes. Also reported are the genetic map locations of 113 novel SSR loci (including four SSR-contg. gene loci) and a linkage map composed of 147 SSR loci and 323 RFLP (restriction fragment length polymorphism) loci. The no. of SSR loci per linkage group ranges from 8 to 30. The SSR loci are distributed relatively evenly throughout approx. 75% of the 1406-cM linkage map, but segments of five linkage groups comprising about 25% of the map either lack or contain few SSR loci. Mapping of SSR loci isolated from BAC clones located to these segments is likely to be the most efficient method for placing SSR loci in the segments.

L1 ANSWER 3 OF 14 CA COPYRIGHT 2003 ACS on STN
TI Methods for constructing DNA library immobilized on microchip
IN Takahashi, Kojiro; Takai, Osamu; Tanga, Michifumi
SO PCT Int. Appl., 32 pp.
CODEN: PIXXD2
PY 2000
2002
AB A method for constructing a cDNA library which comprises hybridizing mRNA with oligo(dT)n on a support and treating with a reverse transcriptase so as to immobilize complementary DNA; or a method for constructing a genomic DNA library which comprises ligating a double-stranded chromosomal DNA library with an oligonucleotide on a support having a restriction enzyme site and then immobilizing the **gDNA library**; a method for prepg. replicas thereof; and a support carrying the thus replicated DNA fragment thereon. Microchips with a DNA library immobilized on are claimed.

L1 ANSWER 4 OF 14 CA COPYRIGHT 2003 ACS on STN
TI Plasmodium vivax merozoite surface protein-3 contains coiled-coil motifs in an alanine-rich central domain
AU Galinski, Mary R.; Corredor-Medina, Claudia; Povoa, Marinette; Crosby, Juan; Ingravallo, Paul; Barnwell, John W.
SO Molecular and Biochemical Parasitology (1999), 101(1,2), 131-147
CODEN: MBIPDP; ISSN: 0166-6851
PY 1999
AB Plasmodium merozoites are covered with a palisade layer of proteins that are arranged as organized bundles or appear as protruding spikes by electron microscopy. Here the authors present a third Plasmodium vivax merozoite surface protein, PvMSP-3, which is assocd. with but not anchored in the merozoite membrane. Serum from a P. vivax immune squirrel monkey was used to screen a .lambda.gt11 P. vivax genomic DNA (**gDNA**) **library**. Plaque-selected antibodies from clone no. 6.1, and rabbit antisera against its encoded protein, produced a pattern in immunofluorescence assays (IFAs) that is consistent with a localization at the surface of mature schizonts and free merozoites. Specific antisera also agglutinated merozoites and recognized a protein of 150 000 Da by SDS-PAGE. The complete msp-3 gene and flanking sequences were cloned from a P. vivax .lambda. Dash II **gDNA library** and also partly characterized by RACE (rapid amplification of cDNA ends). The immediate upstream sequence contains non-coding repeats and a putative protein-encoding open reading frame (ORF), which are also present on the msp-3 5'-RACE gene product. Pvmsp-3 encodes a protein with a calcd. mass of 89 573 Da, which has a potential signal peptide and a major central alanine-rich domain (31%) that exhibits largely .alpha.-helical secondary structure and is flanked by charged regions. The protein does not have a putative transmembrane domain or a consensus sequence for a glycosylphosphatidylinositol (GPI) anchor modification. However, the alanine-rich domain has heptad repeats that are predicted to form coiled-coil tertiary structures, which mediate protein-protein interactions. PvMSP-3 is structurally related to P. falciparum MSP-3 and the 140 000 Da MSP of P. knowlesi. Characterization of PvMSP-3, thus, also begins to define a new interspecies family of evolutionarily related Plasmodium merozoite proteins.

L1 ANSWER 5 OF 14 CA COPYRIGHT 2003 ACS on STN
TI Cloning and complete sequence of the DNA polymerase-encoding gene (BstpolI) and characterization of the Klenow-like fragment from Bacillus stearothermophilus
AU Phang, Seng-Meng; Teo, Chai-Yaw; Lo, Evelyn; Wong, Victor Wong Thi
SO Gene (1995), 163(1), 65-8
CODEN: GENED6; ISSN: 0378-1119
PY 1995
AB A fragment of the DNA polymerase I-encoding gene (polI) from Bacillus stearothermophilus (Bst) was obtained by PCR. This was used as a probe to

obtain a full-length gene from a Bst genomic DNA (**gDNA**) plasmid **library**. Comparison of the sequence to B. caldotenax (Bca) showed about 93% homol. at the amino acid (aa) level. A Klenow-like (BstpolIk) clone was developed and the recombinant protein displayed DNA polymerase activity similar to the wild-type BstPolI enzyme.

L1 ANSWER 6 OF 14 MEDLINE on STN
TI Differential diagnosis of Taenia saginata and Taenia solium infections: from DNA probes to polymerase chain reaction.
AU Gonzalez Luis Miguel; Montero Estrella; Sciutto Edda; Harrison Leslie J S; Parkhouse R Michael E; Garate Teresa
SO TRANSACTIONS OF THE ROYAL SOCIETY OF TROPICAL MEDICINE AND HYGIENE, (2002 Apr) 96 Suppl 1 S243-50.
Journal code: 7506129. ISSN: 0035-9203.
PY 2002
AB The objective of this work was the rapid and easy differential diagnosis of Taenia saginata and T. solium. First, a T. saginata size-selected genomic deoxyribonucleic acid (**gDNA**) **library** was constructed in the vector lambda gt10 using the 2-4 kb fraction from the parasite DNA digested with EcoR1, under 'star' conditions. After differential screening of the library and hybridization analysis with DNA from T. saginata, T. solium, T. taeniaeformis, T. crassiceps, and Echinococcus granulosus (bovine, porcine, and human), 2 recombinant phages were selected. They were designated HDP1 and HDP2. HDP1 reacted specifically with T. saginata DNA, and HDP2 recognized DNA from both T. saginata and T. solium. The 2 DNA probes were then sequenced and further characterized. HDP1 was a repetitive sequence with a 53 bp monomeric unit repeated 24 times in direct tandem along the 1272 bp fragment, while the 3954 bp HDP2 was not a repetitive sequence. Using the sequencing data, oligonucleotides were designed and used in a polymerase chain reaction (PCR). The 2 selected oligonucleotides from probe HDP1 (PTs4F1 and PTs4R1) specifically amplified gDNA from T. saginata, but not T. solium or other related cestodes, with a sensitivity of < 10 pg of T. saginata gDNA, about the quantity of DNA in one taeniid egg. The 3 oligonucleotides selected from the HDP2 sequence (PTs7S35F1, PTs7S35F2, and PTs7S35R1) allowed the differential amplification of gDNA from T. saginata, T. solium and E. granulosus in a multiplex PCR, again with a sensitivity of < 10 pg. These diagnostic tools have immediate application in the differential diagnosis of T. solium and T. saginata in humans and in the diagnosis of dubious cysts in the slaughterhouse. We also hope to apply them to epidemiological surveys of, for example, soil and water in endemic areas.

L1 ANSWER 7 OF 14 MEDLINE on STN
TI An integrated SSR and RFLP linkage map of Sorghum bicolor (L.) Moench.
AU Bhattramakki D; Dong J; Chhabra A K; Hart G E
SO GENOME, (2000 Dec) 43 (6) 988-1002.
Journal code: 8704544. ISSN: 0831-2796.
PY 2000
AB We report the development, testing, and use (for genetic mapping) of a large number of polymerase chain reaction (PCR) primer sets that amplify DNA simple sequence repeat (SSR) loci of Sorghum bicolor (L.) Moench. Most of the primer sets were developed from clones isolated from two sorghum bacterial artificial chromosome (BAC) libraries and three enriched sorghum genomic-DNA (**gDNA**) **libraries**. A few were developed from sorghum DNA sequences present in public databases. The libraries were probed with radiolabeled di- and trinucleotide oligomers, the BAC libraries with four and six oligomers, respectively, and the enriched **gDNA libraries** with four and three oligomers, respectively. Both types of libraries were markedly enriched for SSRs relative to a size-fractionated **gDNA library** studied earlier. However, only 2% of the sequenced clones obtained from the size-fractionated **gDNA library** lacked a SSR, whereas 13% and 17% of the sequenced clones obtained from the BAC and enriched **gDNA libraries**, respectively, lacked a SSR. Primer sets were produced for 313 SSR loci. Two-hundred sixty-six (85%) of the loci

were amplified and 165 (53%) of the loci were found to be polymorphic in a population composed of 18 diverse sorghum lines. (AG/TC)n and (AC/TG)n repeats comprised 91% of the dinucleotide SSRs and 52% of all of the SSRs at the polymorphic loci, whereas four types of repeats comprised 66% of the trinucleotide SSRs at the loci. Primer sequences are reported for the 165 polymorphic loci and for eight monomorphic loci that have a high degree of homology to genes. Also reported are the genetic map locations of 113 novel SSR loci (including four SSR-containing gene loci) and a linkage map composed of 147 SSR loci and 323 RFLP (restriction fragment length polymorphism) loci. The number of SSR loci per linkage group ranges from 8 to 30. The SSR loci are distributed relatively evenly throughout approximately 75% of the 1406-cM linkage map, but segments of five linkage groups comprising about 25% of the map either lack or contain few SSR loci. Mapping of SSR loci isolated from BAC clones located to these segments is likely to be the most efficient method for placing SSR loci in the segments.

L1 ANSWER 8 OF 14 MEDLINE on STN
TI Plasmodium vivax merozoite surface protein-3 contains coiled-coil motifs in an alanine-rich central domain.
AU Galinski M R; Corredor-Medina C; Povoa M; Crosby J; Ingravallo P; Barnwell J W
SO MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (1999 Jun 25) 101 (1-2) 131-47. Journal code: 8006324. ISSN: 0166-6851.
PY 1999
AB Plasmodium merozoites are covered with a palisade layer of proteins that are arranged as organized bundles or appear as protruding spikes by electron microscopy. Here we present a third Plasmodium vivax merozoite surface protein, PvMSP-3, which is associated with but not anchored in the merozoite membrane. Serum from a P. vivax immune squirrel monkey was used to screen a lambdagt11 P. vivax genomic DNA (**gDNA**) **library**. Plaque-selected antibodies from clone no. 6.1, and rabbit antisera against its encoded protein, produced a pattern in immunofluorescence assays (IFAs) that is consistent with a localization at the surface of mature schizonts and free merozoites. Specific antisera also agglutinated merozoites and recognized a protein of 150 000 Da by SDS-PAGE. The complete msp-3 gene and flanking sequences were cloned from a P. vivax lambda Dash II **gDNA library** and also partly characterized by RACE (rapid amplification of cDNA ends). The immediate upstream sequence contains non-coding repeats and a putative protein encoding open reading frame (ORF), which are also present on the msp-3 5'RACE gene product. Pvmsp-3 encodes a protein with a calculated mass of 89 573 Da, which has a potential signal peptide and a major central alanine-rich domain (31%) that exhibits largely alpha-helical secondary structure and is flanked by charged regions. The protein does not have a putative transmembrane domain or a consensus sequence for a glycosylphosphatidylinositol (GPI) anchor modification. However, the alanine-rich domain has heptad repeats that are predicted to form coiled-coil tertiary structures, which mediate protein-protein interactions. PvMSP-3 is structurally related to P. falciparum MSP-3 and the 140000 Da MSP of P. knowlesi. Characterization of PvMSP-3, thus, also begins to define a new interspecies family of evolutionarily related Plasmodium merozoite proteins.

L1 ANSWER 9 OF 14 MEDLINE on STN
TI Molecular cloning and characterization of novel protein kinase gene DYRK3.
AU Xia J; Yang X; Ruan Q; Pan Q; Liu C; Xie W; Deng H
SO CHUNG-HUA I HSUEH I CHUAN HSUEH TSA CHIH, (1998 Dec 10) 15 (6) 327-32. Journal code: 9425197. ISSN: 1003-9406.
PY 1998
AB OBJECTIVE: To isolate full length cDNA of a novel protein kinase and to deduce the protein kinase's classification position and functions. METHODS: cDNA libraries **gDNA library** was screened with a partial cDNA clone which is homologous to human protein kinase DYRK2 as probe. FISH mapping was performed. RESULTS: Two full length cDNAs of a

novel protein kinase from human muscle cDNA library and human testis cDNA library were isolated. The full length cDNA from muscle has an open reading frame which is predicted to encode a protein of 588 amino acid residues and the cDNA from testis to encode a protein of 568 amino acid residues. CONCLUSION: Because the sequence from the 27th codon to the 3' end of the cDNA from muscle is identical to that from the 7th codon to the 3' end of the cDNA from testis, they should be different transcripts of the same gene. As the gene is highly homologous to human protein kinase DYRK2, the present authors termed the gene DYRK3. DYRK3 is homologous to many serine/threonine protein kinases such as yeast Yak1, human Clk1, human Mnb, drosophila melanogaster Mnb and Cdk2. DYRK3 should belong to the Clk family in CMGC group of serine/threonine protein kinase. DYRK3 has been mapped to chromosome 1q32 by FISH.

L1 ANSWER 10 OF 14 MEDLINE on STN
TI Cloning and complete sequence of the DNA polymerase-encoding gene (BstpolI) and characterisation of the Klenow-like fragment from Bacillus stearothermophilus.
AU Phang S M; Teo C Y; Lo E; Wong V W
SO GENE, (1995 Sep 22) 163 (1) 65-8.
Journal code: 7706761. ISSN: 0378-1119.
PY 1995
AB A fragment of the DNA polymerase I-encoding gene (polI) from Bacillus stearothermophilus (Bst) was obtained by PCR. This was used as a probe to obtain a full-length gene from a Bst genomic DNA (**gDNA**) plasmid **library**. Comparison of the sequence to B. caldotenax (Bca) showed about 93% homology at the amino acid (aa) level. A Klenow-like (BstpolIk) clone was developed and the recombinant protein displayed DNA polymerase activity similar to the wild-type BstPolI enzyme.

L1 ANSWER 11 OF 14 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI An integrated SSR and RFLP linkage map of Sorghum bicolor (L.) Moench.
AU Bhattramakki, Dinakar; Dong, Jianmin; Chhabra, Ashok K.; Hart, Gary E. (1)
SO Genome, (December, 2000) Vol. 43, No. 6, pp. 988-1002. print.
ISSN: 0831-2796.
PY 2000
AB We report the development, testing, and use (for genetic mapping) of a large number of polymerase chain reaction (PCR) primer sets that amplify DNA simple sequence repeat (SSR) loci of Sorghum bicolor (L.) Moench. Most of the primer sets were developed from clones isolated from two sorghum bacterial artificial chromosome (BAC) libraries and three enriched sorghum genomic-DNA (**gDNA**) **libraries**. A few were developed from sorghum DNA sequences present in public databases. The libraries were probed with radiolabeled di- and trinucleotide oligomers, the BAC libraries with four and six oligomers, respectively, and the enriched **gDNA libraries** with four and three oligomers, respectively. Both types of libraries were markedly enriched for SSRs relative to a size-fractionated **gDNA library** studied earlier. However, only 2% of the sequenced clones obtained from the size-fractionated **gDNA library** lacked a SSR, whereas 13% and 17% of the sequenced clones obtained from the BAC and enriched **gDNA libraries**, respectively, lacked a SSR. Primer sets were produced for 313 SSR loci. Two-hundred sixty-six (85%) of the loci were amplified and 165 (53%) of the loci were found to be polymorphic in a population composed of 18 diverse sorghum lines. (AG/TC)n and (AC/TG)n repeats comprised 91% of the dinucleotide SSRs and 52% of all of the SSRs at the polymorphic loci, whereas four types of repeats comprised 66% of the trinucleotide SSRs at the loci. Primer sequences are reported for the 165 polymorphic loci and for eight monomorphic loci that have a high degree of homology to genes. Also reported are the genetic map locations of 113 novel SSR loci (including four SSR-containing gene loci) and a linkage map composed of 147 SSR loci and 323 RFLP (restriction fragment length polymorphism) loci. The number of SSR loci per linkage group ranges from 8 to 30. The SSR loci are distributed relatively evenly throughout approximately 75% of the 1406-cM linkage map, but segments of five linkage

groups comprising about 25% of the map either lack or contain few SSR loci. Mapping of SSR loci isolated from BAC clones located to these segments is likely to be the most efficient method for placing SSR loci in the segments.

L1 ANSWER 12 OF 14 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI Plasmodium vivax merozoite surface protein-3 contains coiled-coil motifs in an alanine-rich central domain.
AU Galinski, Mary R. (1); Corredor-Medina, Claudia; Povoa, Marinette; Crosby, Juan; Ingravallo, Paul; Barnwell, John W.
SO Molecular and Biochemical Parasitology, (June 25, 1999) Vol. 101, No. 1-2, pp. 131-147.
ISSN: 0166-6851.
PY 1999
AB Plasmodium merozoites are covered with a palisade layer of proteins that are arranged as organized bundles or appear as protruding spikes by electron microscopy. Here we present a third Plasmodium vivax merozoite surface protein, PvMSP-3, which is associated with but not anchored in the merozoite membrane. Serum from a P. vivax immune squirrel monkey was used to screen a lambdagt11 P. vivax genomic DNA (**gDNA**) **library**. Plaque-selected antibodies from clone no. 6.1, and rabbit antisera against its encoded protein, produced a pattern in immunofluorescence assays (IFAs) that is consistent with a localization at the surface of mature schizonts and free merozoites. Specific antisera also agglutinated merozoites and recognized a protein of 150 000 Da by SDS-PAGE. The complete msp-3 gene and flanking sequences were cloned from a P. vivax lambda Dash II **gDNA library** and also partly characterized by RACE (rapid amplification of cDNA ends). The immediate upstream sequence contains non-coding repeats and a putative protein-encoding open reading frame (ORF), which are also present on the msp-3 5'RACE gene product. Pvmsp-3 encodes a protein with a calculated mass of 89 573 Da, which has a potential signal peptide and a major central alanine-rich domain (31%) that exhibits largely alpha-helical secondary structure and is flanked by charged regions. The protein does not have a putative transmembrane domain or a consensus sequence for a glycosylphosphatidylinositol (GPI) anchor modification. However, the alanine-rich domain has heptad repeats that are predicted to form coiled-coil tertiary structures, which mediate protein-protein interactions. PvMSP-3 is structurally related to P. falciparum MSP-3 and the 140 000 Da MSP of P. knowlesi. Characterization of PvMSP-3, thus, also begins to define a new interspecies family of evolutionarily related Plasmodium merozoite proteins.

L1 ANSWER 13 OF 14 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI Cloning and complete sequence of the DNA polymerase-encoding gene (BstpolI) and characterization of the Klenow-like fragment from Bacillus stearothermophilus.
AU Phang, Seng-Meng; Teo, Chai-Yaw; Lo, Evelyn; Wong, Victor Thi (1)
SO Gene (Amsterdam), (1995) Vol. 163, No. 1, pp. 65-68.
ISSN: 0378-1119.
PY 1995
AB A fragment of the DNA polymerase I-encoding gene (polI) from Bacillus stearothermophilus (Bst) was obtained by PCR. This was used as a probe to obtain a full-length gene from a Bst genomic DNA (**gDNA**) plasmid **library**. Comparison of the sequence to B. caldotenax (Bca) showed about 93% homology at the amino acid (aa) level. A Klenow-like (BstpolIk) clone was developed and the recombinant protein displayed DNA polymerase activity similar to the wild-type BstPolI enzyme.

L1 ANSWER 14 OF 14 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI RFLP-based genetic maps of the homoeologous group 5 chromosomes of bread wheat (Triticum aestivum L.
AU Xie, D. X.; Devos, K. M.; Moore, G.; Gale, M. D. (1)
SO Theoretical and Applied Genetics, (1993) Vol. 87, No. 1-2, pp. 70-74.
ISSN: 0040-5752.

PY 1993
AB Thirty-eight anonymous cDNA and **gDNA** clone sequences from the **libraries** described in Devos etal. (1992) were shown to be located on the homoeologous group 5 chromosomes of wheat by nullisomic-tetrasomic analysis, and 26 of these were mapped. Two further anonymous cDNA markers, Xksu8 and Xksu26 (Kam-Morgan et al. 1989) and the cDNA clones containing the coding regions for ADP-glucose-pyrophorylase (Olive et al. 1989), alpha-amylase-3 (Baulcombe et al. 1987), beta-amylase-1 (Kreis et al. 1987), acyl carrier proteins I and III (Hansen 1987) and II (Hansen and Kauppinen 1991), a ubiquitin activating enzyme (Hatfield et al. 1990), a catalase (Bethards et al. 1987) and a bZlP protein (Guiltinan et al. 1990) also detected sequences on the wheat group 5 chromosomes. The genetic map position of the 18S.26S rDNA locus on the short arm of chromosome 5DS was determined using the clone pTa71 (Gerlach and Bedbrook 1979). The genetic location of a39 (PSR1201), a clone isolated using the ph1b mutant of Sears (1977) and mapping within the deletion on 5BL, was also determined. All DNA markers are presented with their chromosome arm location, copy number and relative hybridization strength in Table 1.

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L1 14 S (GDNA OR SDNA)(6W)LIBR?

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ANSWER 3 OF 14 CA COPYRIGHT 2003 ACS on STN

TI Methods for constructing DNA library immobilized on microchip

IN Takahashi, Kojiro; Takai, Osamu; Tanga, Michifumi

SO PCT Int. Appl., 32 pp.
CODEN: PIXXD2

PY 2000
2002

AB A method for constructing a cDNA library which comprises hybridizing mRNA with oligo(dT)n on a support and treating with a reverse transcriptase so as to immobilize complementary DNA; or a method for constructing a genomic DNA library which comprises ligating a double-stranded chromosomal DNA library with an oligonucleotide on a support having a restriction enzyme site and then immobilizing the **gDNA library**; a method for prepg. replicas thereof; and a support carrying the thus replicated DNA fragment thereon. Microchips with a DNA library immobilized on are claimed.